

Figure 1A

1 AATTCCGGCAGGAGGAAATTCAAGCACTTTTCCTAAAAGAAGGGGAATGGATGCTGAAA 60

61 CAACACGTnTCCCACAAAGGGAGCAGACACTGGGCTTGTGAAGCTGCCCCATACCTTCCC 120

121 CACAGAACTGGGGTCCGGCCTCCCTGACATGCAGATTTCACCCAGAAGACAGAGAAGGA 180

181 GCCAGTGGTCATGGAATGGGCTGGGGTCAAAGACTGGGTGCCTGGGAGCTGAGGCAGCCA 240

241 CCGTTTCAGCCTGGCCAGCCCTCTGGACCCCGAGGTTGGACCCTACTGTGACACACCTAC 300

301 CATGCGGACACTCTTCAACCTCCTCTGGCTTGGCCTGGCCTGCAGCCCTGTTCCACTACT 360

1 M R T L F N L L W L A L A C S P V H T T 20

361 CCTGTCAAAGTCAGATGCCAAAAAGCCGCTCAAAGACGCTGCTGGAGAAGAGTCAGTT 420

21 L S K S D A K K A A S K T L L E K S Q F 40

421 TTCAGATAAGCCGGTGCAAGACCGGGGTTTGGTGGTGACGGACCTCAAAGCTGAGAGTGT 480

41 S D K P V Q D R G L V V T D L K A E S V 60

481 GGTTCCTTGAGCATCGCAGCTACTGCTCGGCAAAGGCCCGGgACAGACACTTTGCTGGGGa 540

61 V L E H R S Y C S A K A R D R H F A G D 80

541 TGTACTGGGCTATGTCACTCCATGGAACAGCCATGGCTACGATGTCACCAAGGTCTTTGG 600

81 V L G Y V T P W N S H G Y D V T K V F G 100

601 GAGCAAGTTCACACAGATCTCACCCGTCTGGCTGCAGCTGAAGAGACGTGGCCGTGAGAT 660

101 S K F T Q I S P V W L Q L K R R G R E M 120

661 GTTTGAGGTCACGGGCCTCCACGACGTGGACCAAGGGTGGATGCGAGCTGTCAGGAAGCA 720

121 F E V T G L H D V D Q G W M R A V R K H 140

721 TGCCAAGGGCCTGCACATAGTGCCTCGGCTCCTGTTGAGGACTGGACTTACGATGATT 780

141 A K G L H I V P R L L F E D W T Y D D F 160

781 CCGGAACGTCTTAGACAGTGAGGATGAGATAGAGGAGCTGAGCAAGACCGTGGTCCAGGT 840

161 R N V L D S E D E I E E L S K T V V Q V 180

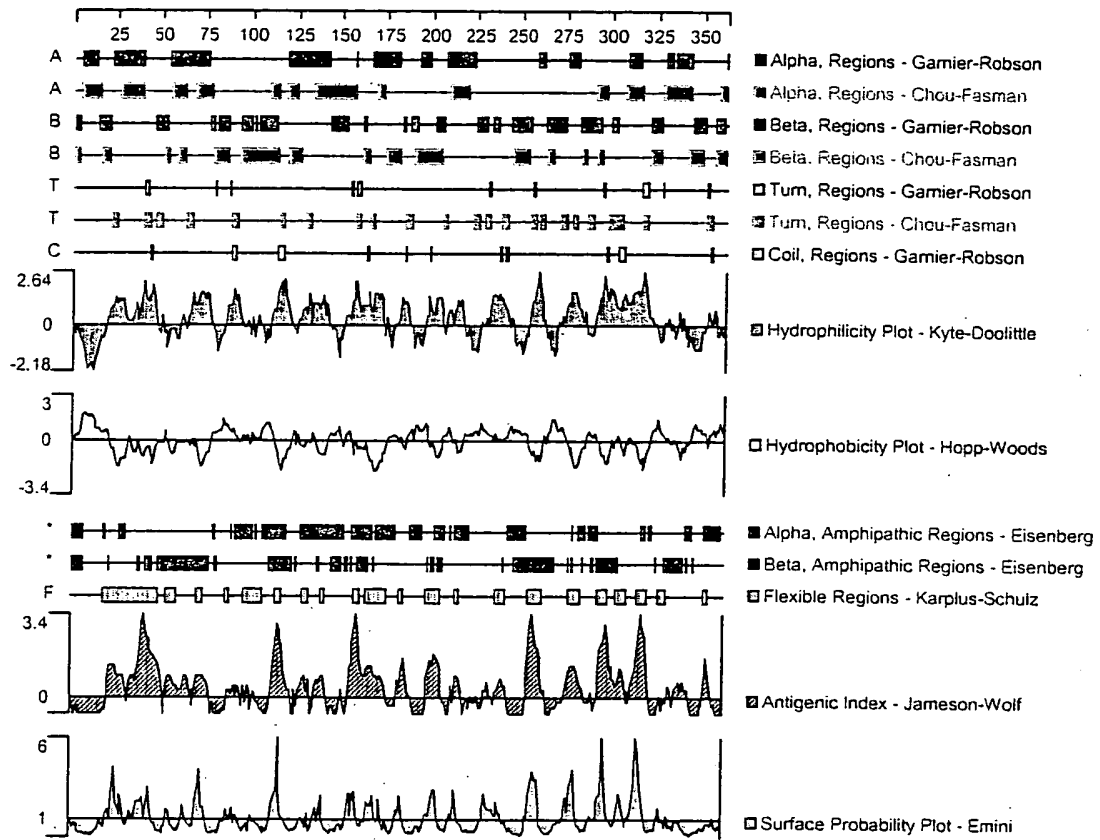
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Figure 1B

841	GGCAAAGAACCAGCATTTTCGATGGCTTCGTGGTGGAGGTCTGGAACCAGCTGCTAAGCCA	900
181	A K N Q H F D G F V V E V W N Q L L S Q	200
901	GAAGCGCGTGACCGACCAGCTGGGCATGTTACGCACAAGGAGTTTGAGCAGCTGGCCCC	960
201	K R V T D Q L G M F T H K E F E Q L A P	220
961	CGTGCTGGATGGTTTCAGCCTCATGACCTACGACTACTCTACAGCGCATCAGCCTGGCCC	1020
221	V L D G F S L M T Y D Y S T A H Q P G P	240
1021	TAATGCACCCCTGTCTGGGTTTCAGCCTGCGTCCAGGTCTTGACCCGAAGTCCAAGTG	1080
241	N A P L S W V R A C V Q V L D P K S K W	260
1081	GCGAAGCAAAATCCTCTGGGGCTCAACTTCTATGGTATGGACTACGCGACCTCCAAGGA	1140
261	R S K I L L G L N F Y G M D Y A T S K D	280
1141	TGCCCCGTGAGCCTGTTGTCTGGGGCCAGGTACATCCAGACACTGAAGGACCACAGGCCCCG	1200
281	A R E P V V G A R Y I Q T L K D H R P R	300
1201	GATGGTGTGGGACAGCCAGGYCTCAGAGCACTTCTTCGAGTACAAGAAGAGCCGAGTGG	1260
301	M V W D S Q X S E H F F E Y K K S R S G	320
1261	GAGGCACGTCGTCTTCTACCCAACCCTGAAGTCCCTGCAGGTGCGGCTGGAGCTGGCCCG	1320
321	R H V V F Y P T L K S L Q V R L E L A R	340
1321	GGAGCTGGGCGTTGGGGTCTCTATCTGGGAGCTGGGCCAGGGCCTGGACTACTTCTACGA	1380
341	E L G V G V S I W E L G Q G L D Y F Y D	360
1381	CCTGCTCTAGGTGGGCATTGCGGCCTCCGCGGTGGACGTGTTCTTTTCTAAGCCATGGAG	1440
361	L L *	362
1441	TGAGTGAGCAGGTGTGAAATACAGGCCTtCACTCCGTTAAAAAAAAAAAAAAAAAAAAA	1500
1501	AAAAAAAAAAAAAA	1515

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Figure 2



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Figure 3A

1	GGCACGAGCCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTTCGGTCAACA	60
61	TCGTAGTCCACCCCCTCCCCATCCCCAGCCCCCGGGATTTCAGGCTCGCCAGCGCCCAGC	120
121	CAGGGAGCCGGCCGGAAGCGCGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCC	180
1	M G A P A A S L L L L L L L	13
181	TGCTGTTTCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCAGGACGGCTACTGGC	240
14	L F A C C W A P G G A N L S Q D G Y W Q	33
241	AGGAGCAGGATTTCGAGCTGGGAACCTCTGGCTCCACTCGACGAGGCCATCAGCTCCACAG	300
34	E Q D L E L G T L A P L D E A I S S S T V	53
301	TCTGGAGCAGCCCTGACATGCTGGCCAGTCAAGACAGCCAGCCCTGGACATCTGATGAAA	360
54	W S S P D M L A S Q D S Q P W T S D E T	73
361	CAGTGGTGGCTGGTGGCACCCTGGTGGCTCAAGTGCCAAGTGAAAGATCACGAGGACTCAT	420
74	V V A G G T V V L K C Q V K D H E D S S	93
421	CCCTGCAATGGTCTAACCCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGAGAGCCCTTC	480
94	L Q W S N P A Q Q T L Y F G E K R A L R	113
481	GAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGCATCAGCA	540
114	D N R I Q L V T S T P H E L S I S I S N	133
541	ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGTGCGAA	600
134	V A L A D E G E Y T C S I F T M P V R T	153
601	CTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTTATA	660
154	A K S L V T V L G I P Q K P I I T G Y K	173
661	AATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAGC	720
174	S S L R E K D T A T L N C Q S S G S K P	193
721	CTGCAGCCCGGCTCACCTGGAGAAAGGTGACCAAGAACTCCACGGAGAACCAACCCGCA	780
194	A A R L T W R K G D Q E L H G E P T R I	213
781	TACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTA	840
214	Q E D P N G K T F T V S S S V T F Q V T	233
841	CCCGGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAG	900
234	R E D D G A S I V C S V N H E S L K G A	253

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Figure 3B

901	CTGACAGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGC	960
254	D R S T S Q R I E V L Y T P T A M I R P	273
961	CAGACCCTCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCA	1020
274	D P P H P R E G Q K L L L H C E G R G N	293
1021	ATCCAGTCCCCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGA	1080
294	P V P Q Q Y L W E K E G S V P P L K M T	313
1081	CCCAGGAGAGTGCCCTGATCTTCCCTTTCTCAACAAGAGTGACAGTGGCACCTACGGCT	1140
314	Q E S A L I F P F L N K S D S G T Y G C	333
1141	GCACAGCCACCAGCAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACC	1200
334	T A T S N M G S Y K A Y Y T L N V N D P	353
1201	CCAGTCCGGTGCCCTCCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTT	1260
354	S P V P S S S S T Y H A I I G G I V A F	373
1261	TCATTGTCTTCTGCTGCTCATCATGCTCATCTTCTCGGCCACTACTTGATCCGGCACA	1320
374	I V F L L L I M L I F L G H Y L I R H K	393
1321	AAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGG	1380
394	G T Y L T H E A K G S D D A P D A D T A	413
1381	CCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCT	1440
414	I I N A E G G Q S G G D D K K E Y F I *	433
1441	AGAGGCGCCTGCCCCACTTCTGCGCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTC	1500
1501	ACCAACCCGGACTTGACAGAGCAACCGAGGGCCGCCCTCCCGCTTGCTCCCCAGCCC	1560
1561	ACCCACCCCCCTGTACAGAATGTCTGCTTTGGGTGCGGTTTTGTACTCGGTTTGGAAATGG	1620
1621	GGAGGGAGGAGGGCGGGGGAGGGGAGGGTTGCCCTCAGCCCTTTCCGTGGCTTCTCTGC	1680
1681	ATTGGGTTATTATTATTTTGTAAACAATCCCAAAGCAAATCTGTCTCCAGGCTGGAGAG	1740
1741	GCAGGAGCCCTGGGGTGAGAAAAGCAAAAACAAAACAAAACCCCTGGAGTGTTA	1800
1801	GGAGGAGAGTGAAGGTAGAGGGGTAGGAAGGGTAAGGGGCAGGGCTGGTTTCAGCTGGG	1860

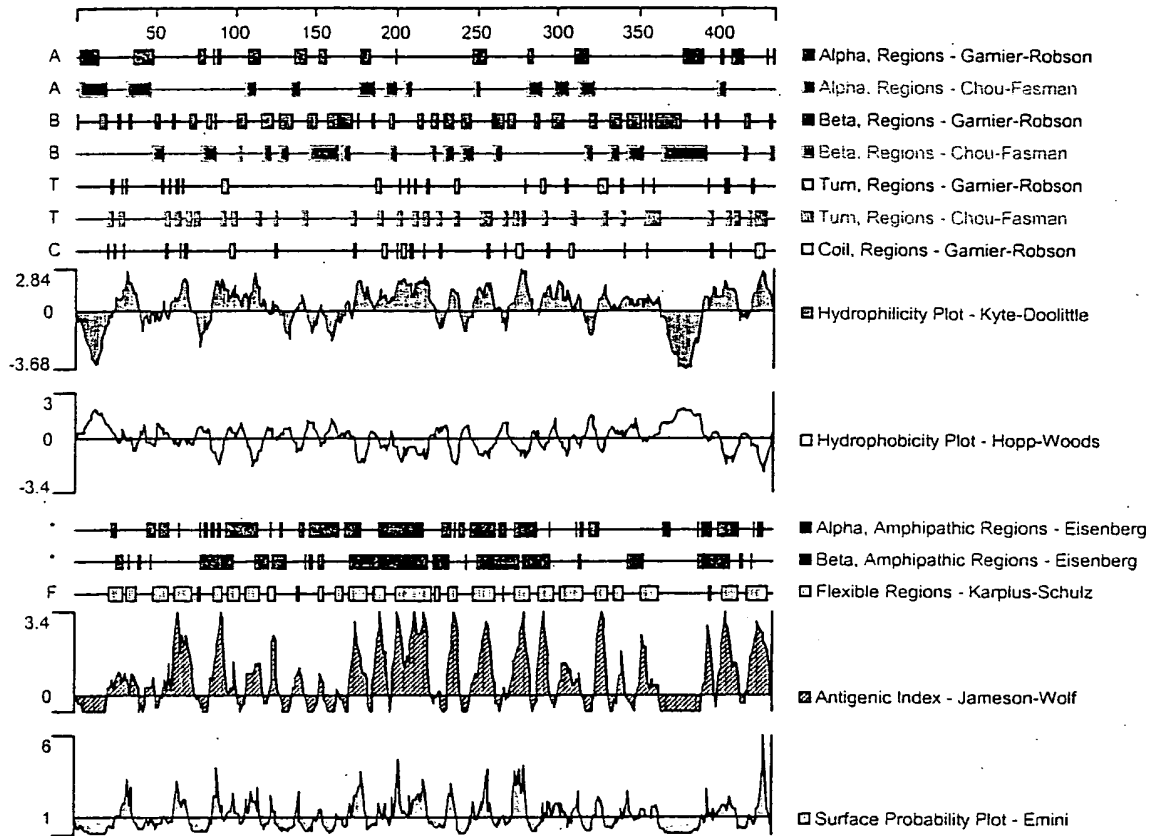
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Figure 3C

1861 GGCTCTCACCAGCCCTCCTTTTCAGCCTCTACAAACAGAGCAGCTTCCCAGACTTCTCCAGG 1920
1921 AACCCAGAAACGGGATGGTTGTTCGGCAAAGGTTGGGAGTGGCTTTTCCTCTGGTAGCCAC 1980
1981 ACACCTGAGCACTACGGACAGGGAGGCAGGTGCCACCTTGACACCTCTCTTCCATAGCAA 2040
2041 TGGGAAAGTGATGAGTGCAGGAGTCTGAGGAGATGTGGCCTGCAGACAACATGCAGCCA 2100
2101 TGCAGGGACCCAGGACTGTAACCTGGGGAGGACGCGGGTCCCTGCAAGGAAGAGTAGATT 2160
2161 TGGAGAGGAAGGATGGAGGTGGACTCTCACCCATTCCCCCGGAAATGAACAAAGCCGG 2220
2221 GCCCTTTCCATAGGAACTGCCCTTGGAGATAGCAGAGTGTGGCTGCCCCCTCCTTGCTCCA 2280
2281 GCAGCAGTGGGAGAGGCACTGCTCTGGGGCCTGAACTGCCTCTGCTTCCCCCCTGAGGG 2340
2341 GCCCCTCACTCTTACCCAAGACTCTGGATTGTTGCACGGCAACCACTCCTCCCATGGCAT 2400
2401 TGCTCAGCAACTACTTCTCCCTTCCCGGCCACCCTGTGCCCCCTTCCTGGTCCCAACGCC 2460
2461 AGCCCTTCATCCTTCCTCCCTCAGCAGCCAGGCAGACATAACAACAAAATACTAAAAGG 2520
2521 AAAAAAAAAAAAAAAAAA 2537

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Figure 4



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Figure 5A

1 CGCCTGGCAC CATGAGGACG CCTGGGCGCTC TGCCTGIGCT GCTGCTGCTC CTGGCGGGAG 60
1 M R T P G P L P V L L L L L A G 16

61 CCCCCGCGC GCGGCCCCACT CCCCCGACCT GCTACTCCCG CATGCGGGCC CTGAGCCAGG 120
17 A P A A R P T P P T C Y S R M R A L S Q 36

121 AGATCACCG CGACTTCAAC CTCCTGCAGG TCTCGGAGCC CTCGGAGCCA TGTGTGACAT 180
37 E I T R D F N L L Q V S E P S E P C V R 56

181 ACCTGCCCAG GCTGTACCTG GACATACACA ATTACTGTGT GCTGGACAAG CTGCGGGACT 240
57 Y L P R L Y L D I H N Y C V L D K L R D 76

241 TTGTGGCCTC GCCCCCGTGT TGGAAAGTGG CCCAGGTAGA TTCCTTGAAG GACAAAGCAC 300
77 F V A S P P C W K V A Q V D S L K D K A 96

301 GGAAGCTGTA CACCATCATG AACTCGTTCT GCAGGAGAGA TTGGTATTTC CTGTTGGATG 360
97 R K L Y T I M N S F C R R D L V F L L D 116

361 ACTGCAATGC CTTGGAATAC CCAATCCCAG TGAATACGGT CCGCCAGAT CGTCAGCGCT 420
117 D C N A L E Y P I P V T T V L P D R Q R 136

421 AAGGGAAGTG AGACCAGAGA AAGAACCCAA GAGAACTAAA GTTATGTCAG CTACCCAGAC 480

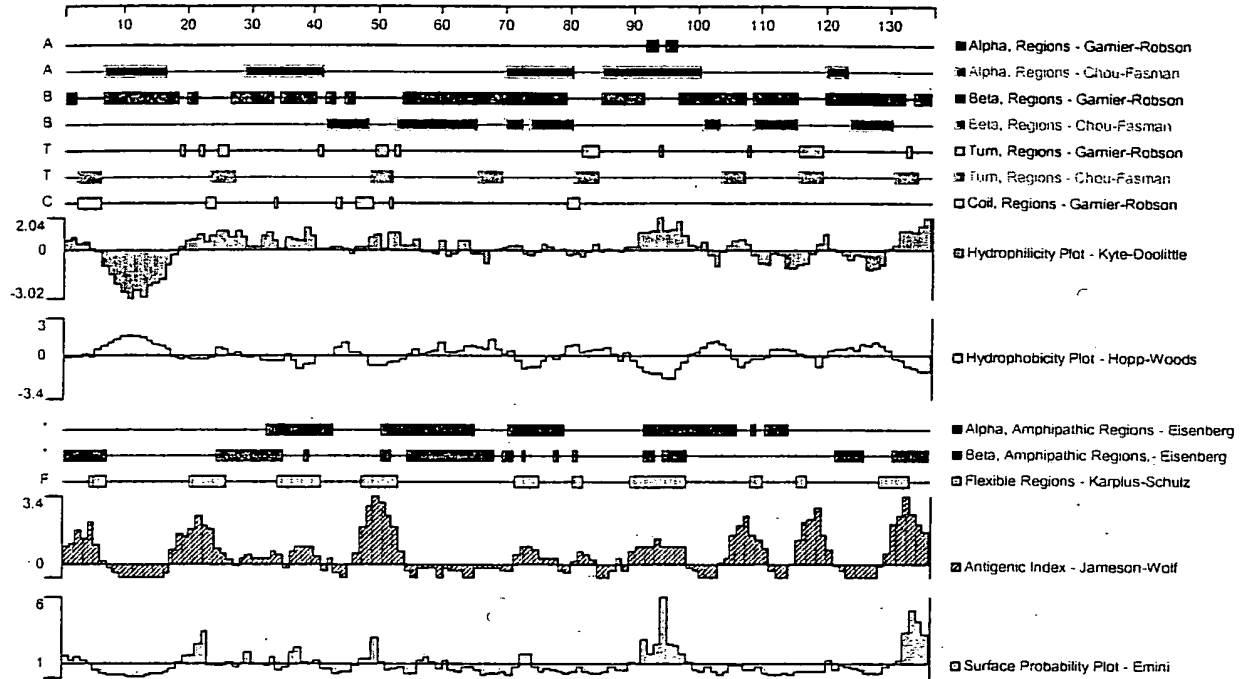
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Figure 5B

481 TTAATGGGCC AGAGCCATGA CCTCACAGG TCTTGIGTGA GTTGTATCTG AAACGTGTAT 540
541 GTATCTCTCT ACCTTCTGGA AAACAGGGCT GGTATTCCTA CCCNGGAACC TCCTTTGAGC 600
601 ATACAGTTAG CAACCATGCT TCTCATTCCC TTGACTCATG TCTTGCCAGG ATGGTTAGAT 660
661 ACACAGCATG TTGATTTGGT CACCTAAAAA GAAGAAAAGG ACTAACAAGC TTCACTTTTA 720
721 TGAACAAC TA TTGAGAAC ATGCACAATA GTATGTTTTT ATTACTGGTT TAATGGAGTA 780
781 ATGGTACITT TATTCTTTCT TGATAGAAAC CTGCTTACAT TTAACCAAGC TTCTATTATG 840
841 CCTTTTTCTA ACACAGACTT TCTTCACTGT CTTTCATTTA AAAAGAAATT AATGCTCTTA 900
901 AGATATATAT TTTAYGTAGT GCTGACAGGA CCCACTCTTT CATGAAAGG TGATGAAAAT 960
961 CAAATAAAGA ATCTCTTCAC ATGARAAAAA AAAAAA 996

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Figure 6



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